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Conference Abstract

# Looking Back for the Future: Utilizing Sawfish Saws from Natural History Collections to Conserve the Critically Endangered Largetooth Sawfish (*Pristis pristis*)

Annmarie Fearing[‡], Kelcee L Smith[§], Tonya R Wiley[|], Jeff M Whitty[¶], Kevin A Feldheim[#], Peter M Kyne[¤], Nicole M Phillips[‡]

‡ University of Southern Mississippi, Hattiesburg, United States of America
§ Louisiana State University, Baton Rouge, United States of America
| Havenworth Coastal Conservation, Palmetto, United States of America
¶ Florida Fish and Wildlife Conservation Commission, Pensacola, United States of America
# Field Museum of Natural History, Chicago, United States of America
¤ Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Australia

Corresponding author: Annmarie Fearing (ann.fearing@eagles.usm.edu), Kelcee L Smith (klswim22@gmail.com), Tonya R Wiley (tonya@havenworth.org), Jeff M Whitty (sawfishconservationsociety@gmail.com), Kevin A Feldheim (kfeldheim@fieldmuseum.org), Peter M Kyne (peter.kyne@cdu.edu.au), Nicole M Phillips (n.phillips@usm.edu)

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## Abstract

The Critically Endangered (International Union for Conservation of Nature) largetooth sawfish, *Pristis pristis*, was historically distributed in the tropical Pacific, Atlantic and Indian Oceans. Today, 'viable' populations are largely limited to northern Australia. Populations that have suffered from drastic declines in abundance, such as those experienced by *P. pristis*, are typically at risk of having reduced, or low, levels of genetic diversity. Previous research found that *P. pristis* in Australia have experienced a genetic bottleneck, but it is unclear whether this bottleneck is the result of contemporary declines over the last century,

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or if it is the result of historic processes. A direct way to assess whether this genetic bottleneck occurred relatively recently is to compare levels of genetic diversity in contemporary and historic populations.

Sawfish saws that were taken as trophies over the past century can now be found in natural history collections around the world and can provide DNA from past sawfish populations. We collected tissue samples from 150 dried *P. pristis* saws found in both private and public natural history collections. Because DNA from natural history specimens tends to be highly degraded, we targeted ten small DNA fragments, ~150 base pairs each, to amplify and sequence the entire mitochondrial control region. These data will provide important baseline information about *P. pristis* that can be used to quantify any loss of genetic diversity over the past ~100 years and assess their long-term survival potential. If the levels of genetic diversity in contemporary populations are severely reduced from those of past populations, protecting remaining genetic diversity within and between viable populations should be a priority in conservation plans.

## Keywords

Sawfish, historic DNA, population bottleneck, genetic diversity, genetic sampling, natural history collections

## Presenting author

Annmarie Fearing